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Hoechst Schering AgrEvo GmbH
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CLAIMS:

1. A transgenic plant comprising transgenic plant cells with a reduced citrate synthase activity in comparison to wild type cells, said plant displaying inhibition of flower formation.
2. The transgenic plant of claim 1, wherein the citrate synthase activity is reduced by inhibiting the expression of DNA sequences which code for citrate synthase.
3. The transgenic plant of claim 2, wherein the inhibition of expression is achieved by the use of antisense RNA.
4. The transgenic plant of claim 2, wherein the inhibition of expression is achieved by the use of ribozymes cleaving specifically RNA coding for citrate synthase.
5. The transgenic plant of any one of claims 1 to 4 which is a useful plant.
6. A storage organ of a plant of any one of claims 1 to 5 comprising cells with a reduced citrate synthase activity.
7. The storage organ of claim 6 which is a tuber.
8. A transgenic plant comprising plant cells which have an increased citrate synthase activity compared to wild type cells because of the additional expression of a DNA sequence which codes for a protein having the enzymatic activity of a citrate synthase, said plant displaying a modified flowering behaviour.

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- (ii) a DNA sequence coding for citrate synthase which is fused to the promoter in sense orientation.

~~17. A vector containing a DNA molecule of claim 15 or 16.~~

18. Plasmid pKS-CSa (DSM 8880).

19. Plasmid TCSAS (DSM 9359).

~~20. Bacteria, containing a DNA molecule of claim 15 or 16 or a vector of any one of claims 17 to 19.~~

~~21. A process for inhibiting flower formation in plants wherein the citrate synthase activity in the cells of the plants is reduced.~~

22. A process to improve the storage capability of storage organs in plants wherein the citrate synthase activity in the cells of the plants is reduced.

23. A process for reducing the sprouting of tubers of transgenic tuberous plants wherein the citrate synthase activity in the cells of the tubers is reduced.

24. The process of any one of claims 21 to 23, wherein the citrate synthase activity is reduced by inhibiting the expression of DNA sequences which code for citrate synthase.

25. The process of claim 24, wherein the expression of DNA sequences which code for citrate synthase is inhibited by the use of anti-sense RNA.

26. The process of claim 25 wherein

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- sequence*
- (a) a DNA₁ which is complementary to a citrate synthase gene present in the cell is stably integrated into the genome of a plant cell;
- (b) ^{*the*} ~~this~~ ^{*sequence*} DNA₁ is expressed constitutively or upon induction due to the combination with suitable elements controlling the transcription;
- (c) the expression of endogenous citrate synthase genes is inhibited because of an anti-sense effect; and
- (d) plants are regenerated from the transgenic cells.

27. The process of claim 25 or 26, wherein the DNA sequence transcribed into anti-sense RNA comprises a nucleotide sequence which codes in sense orientation for a protein having the amino acid sequence given in SeqID No. 1 or SeqID No. 2 or SeqID No. 3 or a DNA sequence which shows a high degree of homology to such a DNA sequence or a part of such sequence wherein the used DNA sequence or part thereof has a length and a degree of homology to an endogenous citrate synthase gene sufficient to elicit an antisense effect and thereby inhibit expression of said endogenous citrate synthase gene.

28. The process of any one of claims 25 to 27, wherein the DNA sequence transcribed into anti-sense RNA comprises the nucleotide sequence given in SeqID No. 1 or SeqID No. 2 or SeqID No. 3, an essentially identical nucleotide sequence or a part thereof or derivatives thereof which are derived by insertion, deletion or substitution of this sequence or a DNA sequence which shows a high degree of homology to such a DNA sequence or a part of such sequence wherein the used DNA sequence or part thereof has a length and a degree of homology to an endogenous citrate synthase gene sufficient to elicit

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an antisense effect and thereby inhibit expression of said endogenous citrate synthase gene.

29. The process of claim 24, wherein the expression of DNA sequences which code for citrate synthase is inhibited by use of ribozymes.

30. A process for inducing flower formation in plants, wherein the citrate synthase activity in the cells of the plant is increased.

31. The process of claim 30, wherein the increase in citrate synthase activity is achieved by expression of a recombinant DNA molecule which is stably integrated into the genome of the plant cells and which comprises the coding region for a citrate synthase and leads to the expression of a citrate synthase in the transformed cells.

32. The process of claim 31, wherein

- (a) DNA which is of homologous or heterologous origin and which codes for a protein having a citrate synthase activity is stably integrated into the genome of a plant cell;
- (b) this DNA is expressed constitutively or upon induction due to the combination with suitable elements controlling the transcription;
- (c) because of this expression the citrate synthase activity in the transgenic cells increases and
- (d) plants are regenerated from the transgenic cells.

33. The process of claim 31 or 32, wherein the DNA sequence comprises a nucleotide sequence which codes for a protein having the amino acid sequence given in SeqID

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No. 1 or SeqID No. 2 or SeqID No. 3 or an essentially identical amino acid sequence or for a part of these sequences wherein the protein encoded by the DNA sequence or the part thereof displays citrate synthase activity.

34. The process of claim 31 or 32, wherein the DNA sequence comprises the nucleotide sequence given in SeqID No. 1 or SeqID No. 2 or SeqID No. 3 or an essentially identical nucleotide sequence or a part thereof, wherein the protein encoded by the DNA sequence or part thereof displays citrate synthase activity.
35. The process of claim 31 or 32, wherein the DNA sequence^{molecule} codes for a deregulated or unregulated citrate synthase.
36. The process of claim 35 wherein the DNA sequence^{molecule} originates from Saccharomyces cerevisiae.
37. The process of claim 35 wherein the DNA sequence^{molecule} originates from a prokaryotic organism.
38. The process of claim 37 wherein the prokaryotic organism is E. coli.
39. Use of DNA sequences which code for citrate synthase (EC No. 4.1.3.7.) for modifying the flowering behaviour of plants.
40. The use of claim 39 wherein the flower formation is inhibited.
41. The use of claim 39 wherein the flower formation is induced.
42. A DNA sequence of a plant of the Solanaceae family or the Chenopodiaceae family which contains the coding

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region for a citrate synthase (EC No. 4.1.3.7.), characterized in that the information contained in the nucleotide sequence permits, upon integration into a plant genome, the formation of transcripts through which an endogenous citrate synthase activity can be suppressed, or permits the formation of transcripts by which the citrate synthase activity in the cells can be increased.

43. The DNA sequence of claim 1, which originates from a plant of the species Solanum tuberosum.
44. The DNA sequence of claim 1, which originates from a plant of the species Nicotiana tabacum.
45. The DNA sequence of claim 1, which originates from a plant of the species sugar beet (Beta vulgaris).
46. The DNA sequence of claim 1, which codes for a protein comprising the amino acid sequence given in SeqID No. 1 or an essentially identical amino acid sequence, said protein having citrate synthase activity.
47. The DNA sequence of claim 1, which codes for a protein comprising the amino acid sequence given in SeqID No. 2 or an essentially identical amino acid sequence, said protein having citrate synthase activity.
48. The DNA sequence of claim 1, which codes for a protein comprising the amino acid sequence given in SeqID No. 3 or an essentially identical amino acid sequence, said protein having citrate synthase activity.
49. The DNA sequence of claim 1, which comprises the nucleotide sequence given in SeqID No. 1 or an

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essentially identical nucleotide sequence which codes for a protein having citrate synthase activity.

50. The DNA sequence of claim 1, which comprises the nucleotide sequence given in SeqID No. 3 or an essentially identical nucleotide sequence which codes for a protein having citrate synthase activity.

51. The DNA sequence of claim 1, which comprises the nucleotide sequence given in SeqID No. 2 or an essentially identical nucleotide sequence which codes for a protein having citrate synthase activity.

52. A plasmid comprising a DNA sequence of any one of claims 42 to 51.

53. Plasmid pPCS (DSM 8879).

54. Plasmid pSBCS (DSM 9385).

55. Plasmid pTCS (DSM 9357).

56. Bacteria, containing a DNA sequence of any one of claims 42 to 51 or a plasmid of any one of claims 52 to 55.

57. Use of a DNA sequence of any one of claims 42 to 51 in combination with control elements for an expression in pro- and eucaryotic cells.

58. Use of a DNA sequence of any one of claims 42 to 51 for the expression of a non-translatable mRNA which prevents the synthesis of an endogenous citrate synthase in the cells.

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59. Use of a DNA sequence of any one of claims 49 to 51 for isolating homologous sequences from the genome of plants.

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